

IN THE CLAIMS:

The claims have been amended as follows:

B2 1. (Currently Amended) An isolated trehalose synthase protein comprising the amino acid sequence as recited in SEQ ID NO: 2 with the following amino acid sequence:

Met	Ser	Ile	Pro	Asp	Asn	Thr	Tyr	Ile	Glu	Trp	Leu	Val	
	Ser	Gln											
				5					10				
	15												
Ser	Met	Leu	His	Ala	Ala	Arg	Glu	Arg	Ser	Arg	His	Tyr	
	Ala	Gly											
				20					25				
	30												
Gln	Ala	Arg	Leu	Trp	Gln	Arg	Pro	Try	Ala	Gln	Ala	Arg	
	Pro	Arg											
				35					40				
	45												
Asp	Ala	Ser	Ala	Ile	Ala	Ser	Val	Trp	Phe	Thr	Ala	Tyr	
	Pro	Ala											
				50					55				
	60												
Ala	Ile	Ile	Thr	Pro	Glu	Gly	Gly	Thr	Val	Leu	Glu	Ala	
	Leu	Gly											
				65					70				
	75												
Asp	Asp	Arg	Leu	Trp	Ser	Ala	Leu	Ser	Glu	Leu	Gly	Val	
	Gln	Gly											
				80					85				
	90												
Ile	His	Asn	Gly	Pro	Met	Lys	Arg	Ser	Gly	Gly	Leu	Arg	
	Gly	Arg											
				95					100				
	105												
Glu	Phe	Thr	Pro	Thr	Ile	Asp	Gly	Asn	Phe	Asp	Arg	Ile	
	Ser	Phe											
				110					115				
	120												
Asp	Ile	Asp	Pro	Ser	Leu	Gly	Thr	Glu	Glu	Gln	Met	Leu	
	Gln	Leu											
				125					130				
	135												
Ser	Arg	Val	Ala	Ala	Ala	His	Asn	Ala	Ile	Val	Ile	Asp	
	Asp	Ile											
				140					145				
	150												
Val	Pro	Ala	His	Thr	Gly	Lys	Gly	Ala	Asp	Phe	Arg	Leu	
	Ala	Glu											
				155					160				
	165												
Met	Ala	Tyr	Gly	Asp	Tyr	Pro	Gly	Leu	Tyr	His	Met	Val	
	Glu	Ile											
				170					175				

Cont  
B2

180	Arg	Glu	Glu	Asp	Trp	Glu	Leu	Leu	Pro	Glu	Val	Pro	Ala
		Gly	Arg										
185													
190													
195	Asp	Ser	Val	Asn	Leu	Leu	Pro	Pro	Val	Val	Asp	Arg	Leu
		Lys	Glu										
200													
205													
210	Lys	His	Tyr	Ile	Val	Gly	Gln	Leu	Gln	Arg	Val	Ile	Phe
		Phe	Glu										
215													
220													
225	Pro	Gly	Ile	Lys	Asp	Thr	Asp	Trp	Ser	Val	Thr	Gly	Glu
		Val	Thr										
230													
235													
240	Gly	Val	Asp	Gly	Lys	Val	Arg	Arg	Trp	Val	Tyr	Leu	His
		Tyr	Phe										
245													
250													
255	Lys	Glu	Gly	Gln	Pro	Ser	Leu	Asn	Trp	Leu	Asp	Pro	Thr
		Phe	Ala										
260													
265													
270	Ala	Gln	Gln	Leu	Ile	Ile	Gly	Asp	Ala	Leu	His	Ala	Ile
		Asp	Val										
275													
280													
285	Thr	Gly	Ala	Arg	Val	Leu	Arg	Leu	Asp	Ala	Asn	Gly	Phe
		Leu	Gly										
290													
295													
300	Val	Glu	Arg	Arg	Ala	Glu	Gly	Thr	Ala	Trp	Ser	Glu	Gly
		His	Pro										
305													
310													
315	Leu	Ser	Val	Thr	Gly	Asn	Gln	Leu	Leu	Ala	Gly	Ala	Ile
		Arg	Lys										
320													
325													
330	Ala	Gly	Gly	Phe	Ser	Phe	Gln	Glu	Leu	Asn	Leu	Thr	Ile
		Asp	Asp										
335													
340													
345	He	Ala	Ala	Met	Ser	His	Gly	Gly	Ala	Asp	Leu	Ser	Tyr
		Asp	Phe										
350													
355													
360	He	Thr	Arg	Pro	Ala	Tyr	His	His	Ala	Leu	Leu	Thr	Gly
		Asp	Thr										
365													
370													
375	Glu	Phe	Leu	Arg	Met	Met	Leu	Arg	Glu	Val	His	Ala	Phe
		Gly	Ile										
380													
385													
390													

Asp	Pro	Ala	Ser	Leu	Ile	His	Ala	Leu	Gln	Asn	His	Asp
	Glu	Leu										
				395					400			
	405											
Thr	Leu	Glu	Leu	Val	His	Phe	Trp	Thr	Leu	His	Ala	Tyr
	Asp	His										
				410					415			
	420											
Tyr	His	Tyr	Lys	Gly	Gln	Thr	Leu	Pro	Gly	Gly	His	Leu
	Arg	Glu										
				425					430			
	435											
His	Ile	Arg	Glu	Glu	Met	Tyr	Glu	Arg	Leu	Thr	Gly	Glu
	His	Ala										
				440					445			
	450											
Pro	Tyr	Asn	Leu	Lys	Phe	Val	Thr	Asn	Gly	Val	Ser	Cys
	Thr	Thr										
				455					460			
	465											
Ala	Ser	Val	Ile	Ala	Ala	Ala	Leu	Asn	Ile	Arg	Asp	Leu
	Asp	Ala										
				470					475			
	480											
Ile	Gly	Pro	Ala	Glu	Val	Glu	Gln	Ile	Gln	Arg	Leu	His
	Ile	Leu										
				485					490			
	495											
Leu	Val	Met	Phe	Asn	Ala	Met	Gln	Pro	Gly	Val	Phe	Ala
	Leu	Ser										
				500					505			
	510											
Gly	Trp	Asp	Leu	Val	Gly	Ala	Leu	Pro	Leu	Ala	Pro	Glu
	Gln	Val										
				515					520			
	525											
Glu	His	Leu	Met	Gly	Asp	Gly	Asp	Thr	Arg	Trp	Ile	Asn
	Arg	Gly										
				530					535			
	540											
Gly	Tyr	Asp	Leu	Ala	Asp	Leu	Ala	Pro	Glu	Ala	Ser	Val
	Ser	Ala										
				545					550			
	555											
Glu	Gly	Leu	Pro	Lys	Ala	Arg	Ser	Leu	Tyr	Gly	Ser	Leu
	Ala	Glu										
				560					565			
	570											
Gln	Leu	Gln	Arg	Pro	Gly	Ser	Phe	Ala	Cys	Gln	Leu	Lys
	Arg	Ile										
				575					580			
	585											
Leu	Ser	Val	Arg	Gln	Ala	Tyr	Asp	Ile	Ala	Ala	Ser	Lys
	Gln	Ile										
				590					595			
	600											
Leu	Ile	Pro	Asp	Val	Gln	Ala	Pro	Gly	Leu	Leu	Val	Met

2. (Currently Amended) An isolated trehalose synthase gene comprising the nucleotide sequence as recited in SEQ ID NO: 1 ~~with the following nucleotide sequence:~~

CGT CTC TGG CAG CGG CGT TAT GCC CAG GCC CGC CCG CGC GAT GCC AGC 1680  
Arg Leu Trp Gln Arg Pro Try Ala Gln Ala Arg Pro Arg Asp Ala Ser

~~GCC ATC GCC TCG GTG TGG TTC ACC GCC TAT CCG GCG GCC ATC ATC ACG~~ 1728  
~~Ala Ile Ala Ser Val Trp Phe Thr Ala Tyr Pro Ala Ala Ile Ile Thr~~

~~CCG GAA GGC GGC ACG GTA CTC GAG GCC CTC GGC GAC GAC CGC CTC TGG~~ 1776  
~~Pro Glu Gly Gly Thr Val Leu Glu Ala Leu Gly Asp Asp Arg Leu Trp~~

~~AGT GCG CTC TCC GAA CTC GGC GTG CAG GGC ATC CAC AAC GGG CCG ATG~~ 1824  
~~Ser Ala Leu Ser Glu Leu Gly Val Gln Gly Ile His Asn Gly Pro Met~~

~~AAG CGT TCC GGT GGC CTG CGC GGA CGC GAG TTC ACC CCG ACC ATC GAC~~ 1872  
~~Lys Arg Ser Gly Gly Leu Arg Gly Arg Glu Phe Thr Pro Thr Ile Asp~~

~~GGC AAC TTC GAC CGC ATC AGC TTC GAT ATC GAC CCG AGC CTG GGG ACC~~ 1920  
~~Gly Asn Phe Asp Arg Ile Ser Phe Asp Ile Asp Pro Ser Leu Gly Thr~~

~~GAG GAG CAG ATG CTG CAG CTC AGC CGG GTG GCC GCG GCG CAC AAC GCC~~ 1968  
~~Glu Glu Gln Met Leu Gln Leu Ser Arg Val Ala Ala Ala His Asn Ala~~

~~ATC GTC ATC GAC GAC ATC GTG CCG GCA CAC ACC GGC AAG GGT GCC GAC~~ 2016  
~~Ile Val Ile Asp Asp Ile Val Pro Ala His Thr Gly Lys Gly Ala Asp~~

~~TTC CGC CTC GCG GAA ATG GCC TAT GGC GAC TAC CCC GGG CTG TAC CAC~~ 2064  
~~Phe Arg Leu Ala Glu Met Ala Tyr Gly Asp Tyr Pro Gly Leu Tyr His~~

~~ATG GTG GAA ATC CGC GAG GAG GAC TGG GAG CTG CTG CCC GAG GTG CCG~~ 2112  
~~Met Val Glu Ile Arg Glu Glu Asp Trp Glu Leu Leu Pro Glu Val Pro~~

~~GCC GGG CGT GAT TCG GTC AAC CTG CTG CCG CCG GTG GTC GAC CGG CTC~~ 2160  
~~Ala Gly Arg Asp Ser Val Asn Leu Leu Pro Pro Val Val Asp Arg Leu~~

~~AAG GAA AAG CAC TAC ATC GTC GGC CAG CTG CAG CGG GTG ATC TTC TTC~~ 2208  
~~Lys Glu Lys His Tyr Ile Val Gly Gln Leu Gln Arg Val Ile Phe Phe~~

~~GAG CCG GGC ATC AAG GAC ACC GAC TGG AGC GTC ACC GGC GAG GTC ACC~~ 2256  
~~Glu Pro Gly Ile Lys Asp Thr Asp Trp Ser Val Thr Gly Glu Val Thr~~

~~GGG GTC GAC GGC AAG GTG CGT CGC TGG GTC TAT CTG CAC TAC TTC AAG~~ 2304  
~~Gly Val Asp Gly Lys Val Arg Arg Trp Val Tyr Leu His Tyr Phe Lys~~

~~GAG GGC CAG CCG TCG CTG AAC TGG CTC GAC CCG ACC TTC GCC GCG CAG~~ 2352  
~~Glu Gly Gln Pro Ser Leu Asn Trp Leu Asp Pro Thr Phe Ala Ala Gln~~

~~CAG CTG ATC ATC GGC GAT GCG CTG CAC GCC ATC GAC GTC ACC GGC GCC~~ 2400  
~~Gln Leu Ile Ile Gly Asp Ala Leu His Ala Ile Asp Val Thr Gly Ala~~

~~CGG GTG CTG CGC CTG GAC GCC AAC GGC TTC CTC GGC GTG GAA CGG CGC~~ 2448  
~~Arg Val Leu Arg Leu Asp Ala Asn Gly Phe Leu Gly Val Glu Arg Arg~~

~~GCC GAG GGC ACG GCC TGG TCG GAG GGC CAC CCG CTG TCC GTC ACC GGC~~ 2496  
~~Ala Glu Gly Thr Ala Trp Ser Glu Gly His Pro Leu Ser Val Thr Gly~~

~~AAC CAG CTG CTC GCC GGG GCG ATC CGC AAG GCC GGC GGC TTC AGC TTC~~ 2544  
~~Asn Gln Leu Leu Ala Gly Ala Ile Arg Lys Ala Gly Gly Phe Ser Phe~~

~~CAG GAG CTG AAC CTG ACC ATC GAT GAC ATC GCC GCC ATG TCC CAC GGC~~ 2592  
~~Gln Glu Leu Asn Leu Thr Ile Asp Asp Ile Ala Ala Met Ser His Gly~~

~~GGG GCC GAT CTG TCC TAC GAC TTC ATC ACC CGC CCG GCC TAT CAC CAT~~ 2640  
~~Gly Ala Asp Leu Ser Tyr Asp Phe Ile Thr Arg Pro Ala Tyr His His~~

~~GCG TTG CTC ACC GGC GAT ACC GAA TTC CTG CGC ATG ATG CTG CGC GAA~~ 2688  
~~Ala Leu Leu Thr Gly Asp Thr Glu Phe Leu Arg Met Met Leu Arg Glu~~

~~GTG CAC GCC TTC GGC ATC GAC CCG GCG TCA CTG ATC CAT GCG CTG CAG~~ 2736  
~~Val His Ala Phe Gly Ile Asp Pro Ala Ser Leu Ile His Ala Leu Gln~~

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*B2*

~~AAC CAT GAC GAG TTC ACC CTG GAG CTG GTG CAC TTC TGG ACG CTG CAC~~ 2784  
~~Asn His Asp Glu Leu Thr Leu Glu Leu Val His Phe Trp Thr Leu His~~

~~GCC TAC GAC CAT TAC CAC TAC AAG GGC CAG ACC CTG CCC GGC GGC CAC~~ 2832  
~~Ala Tyr Asp His Tyr His Tyr Lys Gly Gln Thr Leu Pro Gly Gly His~~

~~CTG CGC GAA CAT ATC CGC GAG GAA ATG TAC GAG CGG CTG ACC GGC GAA~~ 2880  
~~Leu Arg Glu His Ile Arg Glu Glu Met Tyr Glu Arg Leu Thr Gly Glu~~

~~CAC GCG CCG TAC AAC CTC AAG TTC GTC ACC AAC GGG GTG TCC TGC ACC~~ 2928  
~~His Ala Pro Tyr Asn Leu Lys Phe Val Thr Asn Gly Val Ser Cys Thr~~

~~ACC GCC AGC GTG ATC GCC GCG GCG CTT AAC ATC CGT GAT CTG GAC GCC~~ 2976  
~~Thr Ala Ser Val Ile Ala Ala Ala Leu Asn Ile Arg Asp Leu Asp Ala~~

~~ATC GGC CCG GCC GAG GTG GAG CAG ATC CAG CGT CTG CAT ATC CTG CTG~~ 3024  
~~Ile Gly Pro Ala Glu Val Glu Gln Ile Gln Arg Leu His Ile Leu Leu~~

~~GTG ATG TTC AAT GCC ATG CAG CCC GGC GTG TTC GCC CTC TCC GGC TGG~~ 3072  
~~Val Met Phe Asn Ala Met Gln Pro Gly Val Phe Ala Leu Ser Gly Trp~~

~~GAT CTG GTC GGC GCC CTG CCG CTG GCG CCC GAG CAG GTC GAG CAC CTG~~ 3120  
~~Asp Leu Val Gly Ala Leu Pro Leu Ala Pro Glu Gln Val Glu His Leu~~

~~ATG GGC GAT GGC GAT ACC CGC TGG ATC AAT CGC GGC GGC TAT GAC CTC~~ 3168  
~~Met Gly Asp Gly Asp Thr Arg Trp Ile Asn Arg Gly Gly Tyr Asp Leu~~

~~GCC GAT CTG GCG CCG GAG GCG TCG GTC TCC GCC GAA GGC CTG CCC AAG~~ 3216  
~~Ala Asp Leu Ala Pro Glu Ala Ser Val Ser Ala Glu Gly Leu Pro Lys~~

~~GCC CGC TCG CTG TAC GGC AGC CTG GCC GAG CAG CTG CAG CGG CCA GGC~~ 3264  
~~Ala Arg Ser Leu Tyr Gly Ser Leu Ala Glu Gln Leu Gln Arg Pro Gly~~

~~TCC TTC GCC TGC CAG CTC AAG CGC ATC CTC AGC GTG CGC CAG GCC TAC~~ 3312  
~~Ser Phe Ala Cys Gln Leu Lys Arg Ile Leu Ser Val Arg Gln Ala Tyr~~

~~GAC ATC GCT GCC AGC AAG CAG ATC CTG ATT CCG GAT GTG CAG GCG CCG~~ 3360  
~~Asp Ile Ala Ala Ser Lys Gln Ile Leu Ile Pro Asp Val Gln Ala Pro~~

~~GGA CTC CTG GTG ATG GTC CAC GAG CTG CCT GCC GGC AAG GGC GTG CAG~~ 3408  
~~Gly Leu Leu Val Met Val His Glu Leu Pro Ala Gly Lys Gly Val Gln~~

~~CTC ACG GCA CTG AAC TTC AGC GCC GAG CCG GTC AGC GAG ACC ATC TGC~~ 3456  
~~Leu Thr Ala Leu Asn Phe Ser Ala Glu Pro Val Ser Glu Thr Ile Cys~~

~~CTG CCC GGC GTG GCG CCC GGC CCG GTG GTG GAC ATC ATT CAC GAG AGT~~ 3504  
~~Leu Pro Gly Val Ala Pro Gly Pro Val Val Asp Ile Ile His Glu Ser~~

~~GTG GAG GGC GAC CTC ACC GAC AAC TGC GAG CTG CAG ATC AAC CTC GAC~~ 3552  
~~Val Glu Gly Asp Leu Thr Asp Asn Cys Glu Leu Gln Ile Asn Leu Asp~~

~~CCG TAC GAG GGG CTT GCC CTG CGT GTG GTG AGC GCC GCG CCG CCG GTG~~ 3600  
~~Pro Tyr Glu Gly Leu Ala Leu Arg Val Val Ser Ala Ala Pro Pro Val~~

~~ATC TGA GCGC~~  
~~3610~~

Ile

~~ECTCTTCGCG CGCCCCGGGT CCGCCGCTAT AGTGGCAGC GCCTGGGGCG CGCATTCGCC~~ 3670  
~~TGCGCGTCGA GACCAGCCCG TGTCGTTTTC CGCCTTGCAG TGCTGCCGCT~~ 3730  
~~GGCGGTGCTT GCGCACCAG TCTGGGCGCA GACCGCCTGC CCGCCCGGCC AGCAGCCGAT~~ 3790  
~~CTGCCGTAGC GGCAGCTGCC TCTGCGTGCC GGCCGCGGCC AGCGATCCAC AGGCGGTCTA~~ 3850  
~~CGACCGGTC CAGCGTATGG CTACGCTGCC CCTGCAGAAC TGGATCCAGC AGTCGCGCGA~~ 3910  
~~CCGCGTGATG GCGCGCGGCC TCGAGCCGAT ACCGCTGCAG ATCCGCTCGC AGGTCGAGCC~~ 3970  
~~GTATTTTCAT CTTGCCGTGC TGGAGAGTGC GCGGTACCGC GTCGGCGACG AGGTGGTGCT~~ 4030  
~~GACTGCCGCG AACACCCTGC TCGCAACCC GGACGTCAAT GCCGTGACCC TGATCGACGT~~ 4090  
~~CATCGTCTTC CGCCACGAGG AGGATGCCCG GGACAACGTC GCGCTCTGGG CCCATGAGCT~~ 4150

CAAGCACGTC GAGCAATATC TGGACTGGGG CGTCGCCGAG TTCGCCCGGC GCTATACGCA 4210  
 GGATTTCCTT GCCGTGGAGC GCGCGGCTTA TCGGCTGGAG CGTGAGGTGG AAGAGGCCCT 4270  
 GCGCGAGACG CAGACGCGGC GCTGAGCGAG CTGATCGGTG CTGCTGCCCG CACTGGG CTG 4330  
 AAGCCACCA ATGACGCGCG CGAAAACGAA AAACCCCGCC GAGGCGGGGT TTCTGACGCG 4390  
 GGTGTGCGG TCAGCTCAGA ACGCCGGGAC CACGGCGCCC TTGTACTTTT CCTCGATGAA 4450  
 CTGGCGTACT TGCTCGCTGT GCAGCGCGGC AGCCAGTTTC TGCATGGCAT CGCTGTCTTT 4510  
 GTTGTCCGGA CGGGCGACCA GAATGTTTAC GTATGGCGAG TCGCTGCCCT CGATCACCAG 4570  
 GCGGTCCTGG GTCGGGTTCA GCTTGGCTTC CAGCGCGTAG TTGGTGTGA TCAGCGCCAG 4630  
 GTCGACCTGG GTCAGCACGC GCGGCAGAGT CGCGGCTTTC AGTTCGCGGA TCTTGATCTT 4690  
 CTCGGGGTTC TCGGCGATGT CTCGGCGGTG GCGGTGATGC CGGCGCGGTC CTCAGACCG 4750  
 ATC  
 4753]

3. (Original) A recombinant plasmid containing the trehalose synthase gene of claim 1.
4. (Original) The recombinant plasmid according to claim 1 which is recombinant plasmid pCJ122.
5. (Currently Amended) A transformed ~~E. coli~~ E. coli with the recombinant plasmid of claim 1.
6. (Currently Amended) The ~~transformant~~ transformed E. coli according to claim 5 in which the recombinant plasmid is pCJ122.
7. (Original) A process for producing trehalose which comprises reacting the trehalose synthase enzyme of claim 1 with maltose solution to obtain trehalose.
8. (Currently Amended) A process for producing trehalose which comprises ~~crushing~~ lysing the transformed *E. coli* of claim 5, centrifuging the ~~crushed~~ lysed bacteria, and reacting the resulting supernatant with maltose solution to obtain trehalose.
9. (Currently Amended) A ~~new~~ microorganism *Pseudomonas stutzeri* CJ38 that produces trehalose ~~from~~ from maltose.